

SEQUENCE LISTING

<110> FOSTER, Timothy

<120> METHODS FOR TREATING OR PREVENTING INFECTIONS FROM COAGULASE-NEGATIVE STAPHYLOCOCCI

<130> P06335US05/BAS

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<141> 2003-10-21

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<151> 1999-08-31

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<160> 39

<170> PatentIn version 3.1

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144

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192

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240

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288

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Thr Thr Asp Glu Asn Gly Lys Tyr Gln Phe Asp Asn Leu Asp Ser	
1100 1105 1110	
ggt aat tac att att cat ttt gag aaa ccg gaa ggc atg act caa	3384
Gly Asn Tyr Ile Ile His Phe Glu Lys Pro Glu Gly Met Thr Gln	
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Glu Asp Val Arg Val Thr Ile Thr Asp His Asp Asp Phe Ser Ile	
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Thr Val Asn Glu Glu Ser Ile Ala Glu Thr Pro Lys Thr Ser Thr Thr
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 Thr Lys Gln Ala Gln Met Ser Thr Asn Lys Ser Asn Leu Asp Thr Asn
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 Asp Ser Pro Thr Gln Ser Glu Lys Thr Ser Ser Gln Ala Asn Asn Asp
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 Ser Glu Gln Lys Val Tyr Lys Thr Lys Phe Asn Asp Glu Pro Thr Gln
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 Asp Val Glu His Thr Thr Lys Leu Lys Thr Pro Ser Val Ser Thr
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 Asp Ser Ser Val Asn Asp Lys Gln Asp Tyr Thr Arg Ser Ala Val Ala
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 Ser Leu Gly Val Asp Ser Asn Glu Thr Glu Ala Ile Thr Asn Ala Val
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 Ala Ile Ile Ala Glu Ala Leu Lys Lys Asp Phe Ser Asn Pro Asp Tyr
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 Gly Val Asp Thr Pro Leu Ala Leu Asn Arg Ser Gln Ser Lys Asn Ser
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 Pro His Lys Ser Ala Ser Pro Arg Met Asn Leu Met Ser Leu Ala Ala
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 Glu Pro Asn Ser Gly Lys Asn Val Asn Asp Lys Val Lys Ile Thr Asn
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 Pro Thr Leu Ser Leu Asn Lys Ser Asn Asn His Ala Asn Asn Val Ile
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 Trp Pro Thr Ser Asn Glu Gln Phe Asn Leu Lys Ala Asn Tyr Glu Leu
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 Tyr Ile Arg Pro Gly Gly Leu Glu Leu Pro Ala Ile Lys Thr Gln Leu
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Ala Ile Lys Asp Asn Gln Asn Tyr Pro Met Glu Val Thr Ile Ala Asn			
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Glu Val Val Lys Lys Asp Phe Ile Val Asp Tyr Gly Asn Lys Lys Asp			
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Asn Thr Thr Thr Ala Ala Val Ala Asn Val Asp Asn Val Asn Asn Lys			
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His Asn Glu Val Val Tyr Leu Asn Gln Asn Asn Gln Asn Pro Lys Tyr			
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Tyr Ser Leu Gly Asp Tyr Val Trp Leu Asp Lys Asn Lys Asn Gly Val			
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Asp Ser Asn Asn Arg Glu Leu Gln Arg Val Thr Thr Asp Gln Ser Gly			
725	730	735	
His Tyr Gln Phe Asp Asn Leu Gln Asn Gly Thr Tyr Thr Val Glu Phe			
740	745	750	
Ala Ile Pro Asp Asn Tyr Thr Pro Ser Pro Ala Asn Asn Ser Thr Asn			
755	760	765	
Asp Ala Ile Asp Ser Asp Gly Glu Arg Asp Gly Thr Arg Lys Val Val			
770	775	780	
Val Ala Lys Gly Thr Ile Asn Asn Ala Asp Asn Met Thr Val Asp Thr			
785	790	795	800

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 Asp Thr Asn Lys Asp Gly Ile Gln Asp Asp Asn Glu Lys Gly Ile Ser
 820 825 830
 Gly Val Lys Val Thr Leu Lys Asn Lys Asn Gly Asp Thr Ile Gly Thr
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 1400 1405 1410
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 Ser Asp Ser

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1685 1690	1695	
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Ser Lys Gly Thr Leu Leu Gly	Thr Leu Phe Ala Gly	Leu Gly Ala
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  Arg Phe Leu Leu Glu Asn Tyr Ile Glu Ile Val Lys Asp Lys Glu Phe
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Gln Gln Pro Ser His Thr Thr Ile Asn Ser Glu Ala Ser Ile Gln Thr
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Asn Val Asn Ile Ser Gly Asn Gly Asp Glu Gly Ser Thr Ile Ile Asp

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Gln Thr Thr Ile Asn Glu Tyr Thr Gly Glu Phe Arg Thr Ala Ser Tyr			
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Val Asp Lys Asp Gly Ile Gln Asn Thr Asn Asp Asn Glu Lys Pro Leu			
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Ser Asn Val Leu Val Thr Leu Thr Tyr Pro Asp Gly Thr Ser Lys Ser			
625	630	635	640
Val Arg Thr Asp Glu Glu Gly Lys Tyr Gln Phe Asp Gly Leu Lys Asn			
645	650	655	
Gly Leu Thr Tyr Lys Ile Thr Phe Glu Thr Pro Glu Gly Tyr Thr Pro			
660	665	670	
Thr Leu Lys His Ser Gly Thr Asn Pro Ala Leu Asp Ser Glu Gly Asn			
675	680	685	
Ser Val Trp Val Thr Ile Asn Gly Gln Asp Asp Met Thr Ile Asp Ser			
690	695	700	
Gly Phe Tyr Gln Thr Pro Lys Tyr Ser Leu Gly Asn Tyr Val Trp Tyr			
705	710	715	720

Asp Thr Asn Lys Asp Gly Ile Gln Gly Asp Asp Glu Lys Gly Ile Ser
725 730 735

Gly Val Lys Val Thr Leu Lys Asp Glu Asn Gly Asn Ile Ile Ser Thr
740 745 750

Thr Thr Asp Glu Asn Gly Lys Tyr Gln Phe Asp Asn Leu Asn Ser
755 760 765

Gly Asn Tyr Ile Val His Phe Asp Lys Pro Ser Gly Met Thr Gln Thr
770 775 780

Thr Thr Asp Ser Gly Asp Asp Asp Glu Gln Asp Ala Asp Gly Glu Glu
785 790 795 800

Val His Val Thr Ile Thr Asp His Asp Asp Phe Ser Ile Asp Asn Gly
805 810 815

Tyr Tyr Asp Asp Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser
820 825 830

Asp Asp Ser Asp
835 840 845

Ser Asp
850 855 860

Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Gly Leu Asp
865 870 875 880

Asn Ser Ser Asp Lys Asn Thr Lys Asp Lys Leu Pro Asp Thr Gly Ala
885 890 895

Asn Glu Asp His Asp Ser Lys Gly Thr Leu Leu Gly Ala Leu Phe Ala
900 905 910

Gly Leu Gly Ala Leu Leu Gly Lys Arg Arg Lys Asn Arg Lys Asn
915 920 925

Lys Asn
930

<210> 11
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<212> PRT
<213> Staphylococcus epidermidis

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Lys Val Tyr Leu Val Gln Gln Ile
1 5

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Met Lys Lys Phe Asn Ile Lys His Ser Phe Met Leu Thr Gly Phe Ala
1 5 10 15

ttc atg gta act aca tca tta ttc agt cac caa gca cat gct gaa ggt 96
Phe Met Val Thr Thr Ser Leu Phe Ser His Gln Ala His Ala Glu Gly
20 25 30

aat cat cct att gac att aat ttt tct aaa gat caa att gat aga aat 144
Asn His Pro Ile Asp Ile Asn Phe Ser Lys Asp Gln Ile Asp Arg Asn
35 40 45

aca gct aag agc aat att atc aat cga gtg aat gac act agt cgc aca 192
Thr Ala Lys Ser Asn Ile Ile Asn Arg Val Asn Asp Thr Ser Arg Thr
50 55 60

gga att agt atg aat tcg gat aat gat tta gat aca gat atc gtt tca 240
Gly Ile Ser Met Asn Ser Asp Asn Asp Leu Asp Thr Asp Ile Val Ser
65 70 75 80

aat agt gac tca gaa aat gac aca tat tta gat agt gat tca gat tca 288
Asn Ser Asp Ser Glu Asn Asp Thr Tyr Leu Asp Ser Asp Ser Asp Ser
85 90 95

gac agt gac tca gat tca gat agt gac tca gat tca gat agt gac tca 336
Asp Ser Asp Ser
100 105 110

gat tca gat agt gac tca gat tca gac agt gat tca gac tca gat agt 384
Asp Ser Asp Ser
115 120 125

gac tca gat tca gac agt gat tca gac tca gat agt gat tca gat tca 432
Asp Ser Asp Ser

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130	135	140														
gac	agt	gat	tca	gat	tca	gac	agt	gac	tca	gac	agt	gat	tca	480		
Asp	Ser															
145		150			155			155		160						
gat	tca	gat	agt	gat	tca	gat	agt	gat	tca	gat	tca	gat	agt	528		
Asp	Ser															
165			170			175										
gat	tca	gat	tca	gac	agt	gac	tca	gac	agt	gat	tca	gat	tca	576		
Asp	Ser															
180			185			190										
gat	agt	gat	tca	gac	tca	gat	agt	gac	tca	gat	tca	gat	tca	624		
Asp	Ser															
195			200			205										
gac	tct	ggt	aca	agt	tca	ggt	aag	ggt	tca	cat	acc	gga	aaa	aaa	cct	672
Asp	Ser	Gly	Thr	Ser	Ser	Gly	Lys	Gly	Ser	His	Thr	Gly	Lys	Lys	Pro	
210			215				220									
ggt	aac	cct	aaa	gga	aat	aca	aat	aga	cct	tct	caa	aga	cat	acg	aat	720
Gly	Asn	Pro	Lys	Gly	Asn	Thr	Asn	Arg	Pro	Ser	Gln	Arg	His	Thr	Asn	
225			230			235			240							
caa	ccc	caa	agg	cct	aaa	tac	aat	caa	aca	aat	caa	aac	aat	ata	aaa	768
Gln	Pro	Gln	Arg	Pro	Lys	Tyr	Asn	Gln	Thr	Asn	Gln	Asn	Asn	Ile	Asn	
							245		250			255				
aat	ata	aac	cat	aat	att	aat	cat	aca	cgt	act	agt	gga	gat	ggt	gcg	816
Asn	Ile	Asn	His	Asn	Ile	Asn	His	Thr	Arg	Thr	Ser	Gly	Asp	Gly	Ala	
						260		265			270					
cct	ttt	aaa	cgt	caa	caa	aat	att	att	aat	tct	aat	tca	ggt	cat	aga	864
Pro	Phe	Lys	Arg	Gln	Gln	Asn	Ile	Ile	Asn	Ser	Asn	Ser	Gly	His	Arg	
						275		280			285					
aat	caa	aat	aat	ata	aat	caa	ttt	ata	tgg	aac	aaa	aat	ggc	ttt	ttt	912
Asn	Gln	Asn	Asn	Ile	Asn	Gln	Phe	Ile	Trp	Asn	Lys	Asn	Gly	Phe	Phe	
						290		295			300					
aaa	tct	caa	aat	aat	acc	gaa	cat	aga	atg	aat	agt	agc	gat	aat	acc	960
Lys	Ser	Gln	Asn	Asn	Thr	Glu	His	Arg	Met	Asn	Ser	Ser	Asp	Asn	Thr	
						305		310			315			320		
aat	tca	tta	att	agc	aga	ttc	aga	caa	tta	gcc	acg	ggt	gct	tat	aag	1008
Asn	Ser	Leu	Ile	Ser	Arg	Phe	Arg	Gln	Leu	Ala	Thr	Gly	Ala	Tyr	Lys	
						325		330			335					
tac	aat	ccg	ttt	ttg	att	aat	caa	gta	aaa	aat	ttg	aat	caa	tta	gat	1056
Tyr	Asn	Pro	Phe	Leu	Ile	Asn	Gln	Val	Lys	Asn	Leu	Asn	Gln	Leu	Asp	
						340		345			350					
gga	aag	gtg	aca	gat	agt	gac	att	tat	agc	ttg	ttt	aga	aag	caa	tca	1104
Gly	Lys	Val	Thr	Asp	Ser	Asp	Ile	Tyr	Ser	Leu	Phe	Arg	Lys	Gln	Ser	
						355		360			365					
ttt	aga	gga	aat	gaa	tat	tta	aat	tca	tta	caa	aaa	ggg	aca	agc	tat	1152
Phe	Arg	Gly	Asn	Glu	Tyr	Leu	Asn	Ser	Leu	Gln	Lys	Gly	Thr	Ser	Tyr	
						370		375			380					

ttc aga ttt caa tat ttt aat cca ctt aat tct agt aaa tac tat gaa Phe Arg Phe Gln Tyr Phe Asn Pro Leu Asn Ser Ser Lys Tyr Tyr Glu 385 390 395 400	1200
aat tta gat gat cag gtt tta gct tta att aca gga gaa atc ggc tca Asn Leu Asp Asp Gln Val Leu Ala Leu Ile Thr Gly Glu Ile Gly Ser 405 410 415	1248
atg cca gaa ctt aaa aaa cct acg gat aaa gaa gat aaa aat cat agc Met Pro Glu Leu Lys Lys Pro Thr Asp Lys Glu Asp Lys Asn His Ser 420 425 430	1296
gcc ttc aaa aac cat agt gca gat gag ata aca aca aat aat gat gga Ala Phe Lys Asn His Ser Ala Asp Glu Ile Thr Thr Asn Asn Asp Gly 435 440 445	1344
cac tcc aaa gat tat gat aag aaa aag aaa ata cat cga agt ctt tta His Ser Lys Asp Tyr Asp Lys Lys Lys Ile His Arg Ser Leu Leu 450 455 460	1392
tcg tta agt att gca ata att gga att ttt cta gga gtc act gga cta Ser Leu Ser Ile Ala Ile Ile Gly Ile Phe Leu Gly Val Thr Gly Leu 465 470 475 480	1440
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<212> PRT

<213> *Staphylococcus epidermidis*

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Met Lys Lys Phe Asn Ile Lys His Ser Phe Met Leu Thr Gly Phe Ala
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Phe Met Val Thr Thr Ser Leu Phe Ser His Gln Ala His Ala Glu Gly
20 25 30

Asn His Pro Ile Asp Ile Asn Phe Ser Lys Asp Gln Ile Asp Arg Asn
35 40 45

Thr Ala Lys Ser Asn Ile Ile Asn Arg Val Asn Asp Thr Ser Arg Thr
50 55 60

Gly Ile Ser Met Asn Ser Asp Asn Asp Leu Asp Thr Asp Ile Val Ser
65 70 75 80

Asn Ser Asp Ser Glu Asn Asp Thr Tyr Leu Asp Ser Asp Ser Asp Ser
85 90 95

Asp Ser
100 105 110

Asp Ser
115 120 125

Asp Ser
130 135 140

Asp Ser
145 150 155 160

Asp Ser
165 170 175

Asp Ser
180 185 190

Asp Ser
195 200 205

Asp Ser Gly Thr Ser Ser Gly Lys Gly Ser His Thr Gly Lys Lys Pro
210 215 220

Gly Asn Pro Lys Gly Asn Thr Asn Arg Pro Ser Gln Arg His Thr Asn
225 230 235 240

Gln Pro Gln Arg Pro Lys Tyr Asn Gln Thr Asn Gln Asn Asn Ile Asn
245 250 255

Asn Ile Asn His Asn Ile Asn His Thr Arg Thr Ser Gly Asp Gly Ala
260 265 270

Pro Phe Lys Arg Gln Gln Asn Ile Ile Asn Ser Asn Ser Gly His Arg
275 280 285

Asn Gln Asn Asn Ile Asn Gln Phe Ile Trp Asn Lys Asn Gly Phe Phe
290 295 300

Lys Ser Gln Asn Asn Thr Glu His Arg Met Asn Ser Ser Asp Asn Thr
305 310 315 320

Asn Ser Leu Ile Ser Arg Phe Arg Gln Leu Ala Thr Gly Ala Tyr Lys
325 330 335

Tyr Asn Pro Phe Leu Ile Asn Gln Val Lys Asn Leu Asn Gln Leu Asp
340 345 350

: Gly Lys Val Thr Asp Ser Asp Ile Tyr Ser Leu Phe Arg Lys Gln Ser
355 360 365

Phe Arg Gly Asn Glu Tyr Leu Asn Ser Leu Gln Lys Gly Thr Ser Tyr
370 375 380

Phe Arg Phe Gln Tyr Phe Asn Pro Leu Asn Ser Ser Lys Tyr Tyr Glu
385 390 395 400

Asn Leu Asp Asp Gln Val Leu Ala Leu Ile Thr Gly Glu Ile Gly Ser
405 410 415

Met Pro Glu Leu Lys Lys Pro Thr Asp Lys Glu Asp Lys Asn His Ser
420 425 430

Ala Phe Lys Asn His Ser Ala Asp Glu Ile Thr Thr Asn Asn Asp Gly
435 440 445

His Ser Lys Asp Tyr Asp Lys Lys Lys Ile His Arg Ser Leu Leu
450 455 460

Ser Leu Ser Ile Ala Ile Ile Gly Ile Phe Leu Gly Val Thr Gly Leu
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Tyr Ile Phe Arg Arg Lys Lys
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<220>
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18

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<400> 16

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<210> 17
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Leu Pro Xaa Thr Gly
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1 5 10 15

Ala Lys Asp Lys Leu Pro Asp Thr Gly Ala Asn Glu Asp His Asp Ser
20 25 30

Lys Gly Thr Leu Leu Gly Thr Leu Phe Ala Gly Leu Gly Ala Leu Leu
35 40 45

Leu Gly Arg Arg Arg Lys Lys Asp Asn Lys Glu Lys
50 55 60

<210> 19
<211> 60
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<213> Staphylococcus epidermidis

<400> 19

Ser Asp Ser Asp Ser Asp Ser Gly Leu Asp Asn Ser Ser Asp Lys Asn
1 5 10 15

Thr Lys Asp Lys Leu Pro Asp Thr Gly Ala Asn Glu Asp His Asp Ser
20 25 30

Lys Gly Thr Leu Leu Gly Ala Leu Phe Ala Gly Leu Gly Ala Leu Leu
35 40 45

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: Leu Gly Lys Arg Arg Lys Asn Arg Lys Asn Lys Asn
  50          55          60

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Asp Lys Asn His Ser Ala Phe Lys Asn His Ser Ala Asp Glu Ile Thr
1           5           10          15

Thr Asn Asn Asp Gly His Ser Lys Asp Tyr Asp Lys Lys Lys Ile
20          25          30

His Arg Ser Leu Leu Ser Leu Ser Ile Ala Ile Ile Gly Ile Phe Leu
35          40          45

Gly Val Thr Gly Leu Tyr Ile Phe Arg Arg Lys Lys
50          55          60

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caggaggcaa gtcacacctg                                19

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gccggatccc caattccaga ggattca                                27

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: gccaaagctta ttgttagaac ctgactc          27

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cccgaaattct agttttcag gaggcaagtc acc 33

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<210> 36
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Gly Gly Ala Gly
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<210> 38
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<212> PRT
<213> *Staphylococcus aureus*

<400> 39

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